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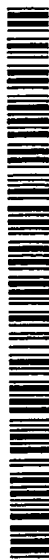


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(54) Title: GENETIC SCREENING METHODS

(57) Abstract: A screening method which applies the principle of synthetic lethality to a gene of interest in mammalian cells. The method may be used to screen either a chemical library in order to identify a molecule having a gene-specific lethal property in the cells, or to screen a group of DNA molecules in order to identify among them one or more modulators of gene function which are synergistically lethal to the cells together with an incapacitated gene of interest. Also described are episomal survival plasmids and kits which may be used with the method.

GENETIC SCREENING METHODS

FIELD OF THE INVENTION

This invention relates to genetic screening methods useful in isolating genes and identifying unknown functions of genes or unknown functional links between genes as well as in identifying molecules having gene-specific lethal properties.

BACKGROUND OF THE INVENTION

The following publications may be relevant to the understanding of the invention, and are referred to in the specification by number:

1. Bender and J.R. Pringle, *Mol. Cell. Biol.* **11**, 1295 (1991);
- 10 2. V. Doye and E.C. Hurt, *Trends Genetics* **11**, 235 (1995);
3. Koshland, D. *et al*, *Cell* **40**, 393 (1985);
4. Davies A.G., *et al*, *Genetics* **153**, 117 (1999).

With continued progress in the Human Genome Project as well as the initiation of the Mouse/Rat Genome Projects, and the sequencing of the majority of the human cDNAs, the elucidation of gene function has become a major priority. High throughput screening methods are required in order to determine the functions of large numbers of genes in an efficient manner.

Screening methods are also required for discovering novel gene-specific drugs. In the search for such drugs, it would be advantageous to be able to elucidate the interaction between specific chemical reagents and

one or more genes in a high throughput format. This is particularly relevant with respect to cancer drugs.

A synthetic or synergistic lethality screening method has previously been described in yeast cells (1,2). The essence of this screen in yeast, is the
5 ability to identify nonallelic and nonessential mutation/s that are lethal in combination with a nonessential mutation in a gene of interest (i.e. synthetic lethality). A wild-type copy of the gene of interest, on an episomal plasmid, is introduced into cells which are null for expression of this gene. Random chemical mutagenesis of the entire yeast genome within these cells may
10 inactivate a gene which is synthetically lethal with the gene of interest. Under these conditions, retention of the episomal plasmid, which is otherwise spontaneously lost, and expression of the gene of interest become essential for survival (i.e. survival plasmid). Plasmid loss or retention is detected by changes in colony pigmentation, due to the presence on the plasmid of a
15 wild-type gene whose product is essential for red pigment accumulation (3). This genetic method is very powerful as it can reveal not only interactions between gene products with direct physical contacts, but also interactions along the same or parallel pathways.

A genetic synthetic lethality screen modeled after the yeast method has
20 recently been described in nematodes (4).

A synthetic lethality screen in mammalian cells in general and in human cells in particular, has not yet been described.

SUMMARY OF THE INVENTION

In an effort to expand the arsenal of genetic tools which can be applied
25 to other eukaryotic biological systems, it has now been discovered that the concept of the yeast synthetic lethality screen can be applied to mammalian cells and particularly to human cells.

An object of the present invention is to provide a screening method useful in identifying molecules such as drug compounds having gene-specific cell-lethal properties.

A further object of the present invention is to provide a screening
5 method useful in isolating genes and identifying unknown functions of genes or unknown functional links between genes.

In a first aspect of the invention, there is provided a method for screening a chemical library comprising a plurality of molecule types in mammalian cells having a genome, in order to identify a molecule type
10 having a gene-specific lethal property in the cell, the genome comprising a gene of interest which carries a non-lethal mutation therein.

The method comprises the following steps:

- (a) transfecting a first reporter gene into the cells, and selecting clones stably expressing the reporter gene;
- 15 (b) introducing into the cells an episome comprising a functioning copy of the gene of interest, a second reporter gene, a dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within the cells, wherein the episome is spontaneously lost from the cells, and growing the cells
20 in the presence of a selection compound which selects for the dominant selectable marker;
- (c) selecting cell clones stably expressing the second reporter gene and the functioning copy of the gene of interest;
- (d) seeding of the cells into a plurality of cell chambers and
25 removing the selection compound;
- (e) adding a molecule type of the chemical library to each of the plurality of cell chambers, measuring expression of the first and second reporter genes in the chambers, and calculating the ratio of the

measured expressions, thereby indicating retention of the episome;
and

- (f) identifying a cell chamber in which the episome is retained,
thus identifying a molecule type having a mutant gene-specific lethal
property in the cell.

In this aspect of the invention, chemical reagent induced synthetic lethality (i.e. chemical synthetic lethality) identifies biochemical inhibitors or drugs whose lethal effect is dependent on the full or partial inactivation of a specific gene (i.e. gene of interest) within its cellular milieu.

- In an alternate embodiment of this aspect of the invention, there is provided a method for screening a chemical library comprising a plurality of molecule types in mammalian cells having a genome, in order to identify a molecule type having a gene-specific lethal property in the cell, the cell expressing the gene of interest. The gene of interest may have a wild-type or mutated genotype, which is either expressed at normal levels or overexpressed. In this specification, expression of the gene of interest includes all of these possibilities.

The method comprises the following steps:

- (a) transfecting a first reporter gene into the cells, and selecting clones stably expressing the reporter gene;
- (b) introducing into the cells an episome comprising a dominant-negative mutant of the gene of interest, a second reporter gene, a dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within the cells, wherein the episome is spontaneously lost from the cells, and growing the cells in the presence of a selection compound which selects for the dominant selectable marker;
- (c) selecting cell clones stably expressing the second reporter gene and the dominant-negative mutant of the gene of interest;

(d) seeding of the cells into a plurality of cell chambers and removing the selection compound;

(e) adding a molecule type of the chemical library to each of the plurality of cell chambers, measuring expression of the first and second reporter genes in the chambers, and calculating the ratio of the measured expressions, thereby indicating retention of the episome; and

(f) identifying a cell chamber in which the episome is retained, thus identifying a molecule type having a gene-specific lethal property in the cell.

In a second aspect of the invention, there is provided a method for screening a collection of DNA molecules selected from the group consisting of antisense cDNA, truncated cDNA, DNA encoding interfering RNA (RNAi) (dsRNA or RNA having inverted repeat), full-length cDNA and genomic DNA, (or any other DNA form) in order to identify from among them one or more modulators of gene function which are synergistically lethal to a mammalian cell together with an incapacitated gene of interest, the cell having a genome which comprises the incapacitated gene of interest.

The method of this aspect of the invention comprises the following steps:

(a) transfecting a first reporter gene into the cell, and selecting clones stably expressing the reporter gene;

(b) introducing into the cells an episome comprising a functioning copy of the gene of interest, a second reporter gene, a first dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within the cells, wherein the episome is spontaneously lost from the cells, and growing the cells in the presence of a selection compound which selects for the first dominant selectable marker;

(c) selecting cell clones stably expressing the second reporter gene and the functioning copy of the gene of interest;

(d) incorporating each of the DNA molecules into vector vehicles containing a second dominant selectable marker gene;

5 (e) transfecting the cells with the vector vehicles so that each transfected cell contains on the average approximately one to several of the molecules, and allowing expression of the molecules in the cells;

10 (f) seeding the transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, and initiating conditions for selection of the second dominant marker, while removing the selection compound for the first dominant selectable marker;

15 (g) measuring expression of the first and second reporter genes in the chambers, and calculating the ratio of the measured expressions, thereby indicating retention of the episome; and

(h) identifying a cell chamber in which the episome is retained, thus identifying a DNA molecule which is a modulator of gene function.

20 In a further embodiment of this aspect of the invention, there is provided a method for screening a collection of DNA molecules selected from the group consisting of antisense cDNA, truncated cDNA, DNA encoding RNAi, full-length cDNA, genomic DNA, or any other DNA form in order to identify among them one or more modulators of gene function which are
25 synergistically lethal to a mammalian cell, the cell having a genome which expresses the wild-type gene of interest.

The method of this embodiment comprises the following steps:

(a) transfecting a first reporter gene into the cell, and selecting clones stably expressing the reporter gene;

- 5 (b) introducing into the cells an episome comprising a dominant-negative mutant of the gene of interest, a second reporter gene, a first dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within the cells, wherein the episome is spontaneously lost from the cells, and growing the cells in the presence of a selection compound which selects for the first dominant selectable marker;
- (c) selecting cell clones stably expressing the second reporter gene and the dominant-negative mutant of the gene of interest;
- 10 (d) incorporating each of the DNA molecules into vector vehicles containing a second dominant selectable marker gene;
- (e) transfecting the cells with the vector vehicles so that each transfected cell contains on the average approximately one to several of the molecules, and allowing expression of the molecules in the cells;
- 15 (f) seeding the transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, and initiating conditions for selection of the second dominant marker, while removing the selection compound for the first dominant selectable marker;
- 20 (g) measuring expression of the first and second reporter genes in the chambers, and calculating the ratio of the measured expressions, thereby indicating retention of the episome; and
- (h) identifying a cell chamber in which the episome is retained, thus identifying a DNA molecule which is a modulator of gene function.
- 25

In this aspect of the invention, synthetic lethality imposed by either a GSE (defined below) or by an overexpressed full-length cDNA (i.e. genetic synthetic lethality) identifies gene function or functional links between genes.

The following terms used in the present specification have the indicated definitions:

non-essential gene – a gene whose function is non-essential to the viability of the cell, either because it is dispensible for cell metabolism or due
5 to the existence of one or more other genes which functionally overlap with it.

non-lethal mutation – a mutation within a non-essential gene or a defect within an essential gene which is partial and thus leaves the cell viable.

gene of interest – a specific gene which is either non-essential for viability or an essential gene carrying a non-lethal mutation. Its function may
10 be known or unknown.

synthetic or synergistic lethality – a lethal cell phenotype which is the result of either the synergistic incapacitation of two (or more) genes, or due to the overexpression of one gene on the background of the incapacitation of the gene of interest and *vice versa*. Either one of these two conditions may also
15 require the overexpression and/or underexpression of other gene(s). The incapacitation of activity may be full or only partial. The incapacitation may be as a result of a resident mutation, or due to an externally inserted element, such as a truncated cDNA, an antisense cDNA molecule or a chemical reagent.

20 *Episomal survival plasmid* – a gene vehicle/vector which carries either a functioning copy or a dominant-negative mutant of a gene of interest. The plasmid is not incorporated into the genome of the cell, and yet can autonomously replicate within the cell (i.e. an episome). The episome includes an origin of DNA replication which may be of viral or mammalian
25 origin, and a nuclear antigen gene. The plasmid is spontaneously gradually lost from the cell population.

genetic suppressor element (GSE) – a nucleic acid capable of suppressing genetic expression in a dominant-negative fashion. Examples of GSEs are antisense cDNA, truncated sense cDNA, DNA encoding RNAi

and other forms of mutated DNA. These encode antisense RNAs, dsRNAs or RNAs having inverted repeats (both belonging to the RNAi type), RNA aptamers, ribozymes, peptide aptamers, or truncated polypeptides.

modulators of gene expression – a group of DNA molecules which
5 affect gene expression of the host cells. These DNA molecules are either GSEs or overexpressed wild-type genes.

vector vehicles for modulators of gene expression – a group of vectors containing among others: episomal mammalian expression vectors, retroviral vectors, other RNA-based viral vectors, DNA viral vectors and chimeric
10 transposable element vectors.

chemical library – a group of different chemical reagents which may comprise synthetic as well as natural compounds. Each of the different types of reagents may be referred to at times as '*molecule types*'. This definition also includes, but is not limited to, drug compounds, synthetic antisense DNA
15 oligonucleotides which may also be modified (phosphorothioate antisense oligodeoxynucleotides, chimeric oligodeoxynucleotides, etc.).

The method of the invention is based on the screening of a cell population for either loss of gene function or gene overexpression resulting in lethality. The survival plasmid carries the genetic information which is
20 necessary for cell survival under the specific conditions of the imposed synthetic lethality. This results in a strong selective advantage for retaining the episomal survival plasmid which would otherwise be lost from the cell. In this manner, the phenotype of lethality may be identified by the maintenance of the plasmid in an otherwise non-viable cell.

25 Synthetic lethality is dependent on two independent events of gene incapacitation. or a combination of the incapacitation of the gene of interest, and overexpression of the other gene in its non-mutated form, and *vice versa*. The gene incapacitation may be either by genetic means or by an external specific chemical inhibitor. Thus, if the nature of one of the events is known,

the nature of the other event can be surmised as being overlapping, complementing or antagonizing the first event. In this way, an unknown function may be identified.

The method of the invention differs from the synthetic lethality screen
5 previously described in yeast in the following respects:

(1) Synthetic lethality as disclosed in yeast is recognized by the visible color of yeast colonies grown on agar within petri dishes. The majority of colonies exhibit the appearance of white sectors within red colonies, while a synthetic lethal condition prevents the appearance of white sectors in a
10 primarily red colony. The accumulation of red pigment is enabled by the reporter gene acting together with other genes.

In contrast, the method of the invention involves the seeding of human/mammalian cells into microtiter plates, and the periodic measurement in a fluorescent plate reader of the double-label fluorescent ratio of two
15 fluorescent proteins. Retention over time of a high ratio in the readings of a fluorescent variant encoded by the survival plasmid to a second fluorescent variant produced from a chromosomally integrated gene, indicates selection for maintenance of the survival plasmid and thus a synthetic lethality condition. The fluorescence is a direct product of the reporter gene.

20 (2) Synthetic lethality is imposed in yeast by randomly mutagenizing the whole yeast genome with a chemical mutagen, thus leading to random gene inactivation. In contrast, in the present invention, synthetic lethality is achieved by either a chemical inhibitor (chemical synthetic lethality) or a genetic incapacitation (genetic synthetic lethality). The latter involves
25 overexpressing full-length sense cDNA libraries or GSE libraries, either one of which is incorporated into episomal plasmids (J.L. Yates, N. Warren and B. Sugden, Nature 313, 812 (1985); L.P. Deiss and A. Kimchi, Science 252, 117 (1991)), retroviral vectors (A.V. Gudkov et al., Proc. Natl. Acad. Sci. USA

90, 3231 (1993)), other RNA- or DNA- viral vectors, or chimeric transposable elements (Z. Ivics *et al* , Cell 91,501 (1997)).

(3) Identification of the gene which is synthetic lethal with the gene of interest is performed in yeast by first isolating those colonies in which the red pigment was maintained and no white sectors appear. Those colonies putatively harbor a chromosomally mutated gene which is synthetic lethal with the gene of interest. Those yeast colonies are transfected by a normal yeast genomic library incorporated into a yeast multi-copy plasmid. Those transformants transfected by and expressing a wild-type copy of the chromosomally mutated gene, no longer sustain a synthetic lethality condition. and therefore no longer need to retain the survival plasmid. Those few colonies are recognized by the appearance of white sectors, from which the plasmid DNA is extracted, transformed into bacteria and further analyzed for the identity of the yeast gene insert by standard recombinant DNA methods.

Identification of the genetic element which confers the synthetic lethal phenotype in human/mammalian cells of the present invention, on the other hand, does not require a further transfection with a normal gene/cDNA library. This is because, unlike in the yeast method, gene incapacitation is not achieved by mutagenizing the endogenous resident cell genome but rather by an exogenous DNA element working either in a dominant-negative fashion or by overexpression of a wild-type cDNA. Accordingly, the external genetic element conferring the synthetic lethality is recovered by either one of two approaches, depending on the type of vector/vehicle used: (a) an episomal plasmid, or chimeric RNA or DNA based viral replicons are rescued by Hirt supernatant-extract mediated bacterial transformation or purification of packaged virus-like particles, respectively; (b) chromosomally integrated GSE or a wild-type sense cDNA library incorporated into either a retroviral vector or a chimeric transposable element, are recovered by PCR on genomic DNA.

The availability of a large number of mutant human cell lines derived from genetic disorders on the one hand, and the ability to employ homologous recombination for gene disruption in somatic human cells on the other, constitutes a large reservoir of recipient cells and genes of interest.

5 The cells which may be used in the method of the invention are mammalian cells. Preferably they are human cells, but the same principle may be applied to e.g., rodent cells harboring a survival plasmid with the appropriate replication properties.

10 The survival plasmid contains a reporter gene so as to enable determination of the presence of the plasmid in the cells. The product of the reporter gene may be any detectable molecule, such as the following biosensors: luciferin (luciferase substrate); aequorin; Fluo-3/acetoxymethyl (esterase substrate); FDG (β -gal substrate); or CCF2 which is a β -lactamase substrate [J.E. González and P.A. Negulescu, Curr. Opin. Biotechnol. 9, 624
15 (1998)]. Preferably, the reporter gene encodes a fluorescent protein whose expression can be distinguished from that of a second fluorescent protein marking the cell number. Non overlapping excitation or emission spectra of the two fluorescent proteins allows for double-label fluorescence measurement.

20 Accordingly the cells are also made to incorporate in their genome a second reporter gene which indicates the number of cells. By comparing the signals obtained from the two reporter genes, a relative ratio between the number of survival plasmids and the number of cells may be determined.

25 The methods of the invention may be carried out using conventional systems for growing, scanning and sorting cells, such as microtiter plates, 96-well, 384-well or other high-density microplates, a microplate fluorescent reader, and a fluorescent activated cell sorter (FACS). The methods are especially useful in high throughput screening, where automation allows for

the rapid screening of large number of chemicals as well as the full spectrum of mammalian genes and their respective GSEs.

The present invention may be used in a number of applications.

The first aspect of the invention should prove advantageous in the
5 search of drugs which synergize with particular gene deficiencies or gene status to cause cell lethality as well as identifying drug compounds having gene-specific lethal properties. A special application of this aspect would be to look for chemicals which kill either a benign or cancerous cell growth in a defined genetic milieu where the chemical is synthetic lethal with a particular
10 mutant gene.

The second aspect of the invention is useful in identifying human genes whose under or over-expression causes lethality of human cell lines with defined genetic abnormalities. Such genes are obviously potential targets for drugs aimed at eliminating the affected cells/tissue. The application of this
15 approach to human tumor-derived cell lines, is particularly amenable to identification of targets for cancer therapy.

Above and beyond the identification of gene targets of therapeutic interest in defined genetic background, the invention should prove useful as a tool for basic research. In particular, the invention may enable researchers to
20 rapidly screen large sets of gene products for functional interactions and helps define genetic pathways within the cell (2).

The method using rodent cells should be useful as a model for human genetic traits and responses in drug development and disease research. For example, mutant mice generated by either homologous recombination or
25 tagged random mutagenesis, supply a large source of recipient mutated mouse embryo fibroblasts which, together with the methods of the invention, will greatly facilitate research and development of new drugs and therapeutic strategies for human beings.

Also included in the invention are kits for synthetic lethality screening. One such kit in accordance with the first aspect of the invention would preferably include an episomal survival plasmid and an integrating vector, each carrying a reporter gene, for a chemical synthetic lethality screen. A kit
5 in accordance with the second aspect of the invention would preferably include the above genetic elements together with a library of GSEs or sense cDNAs incorporated within an extrachromosomal vector.

DETAILED DESCRIPTION OF THE DRAWINGS:

In order to understand the invention and to see how it may be carried
10 out in practice, a preferred embodiment will now be described, by way of non-limiting example only, with reference to the accompanying drawings, in which:

Fig. 1 illustrates *de novo* and salvage pathways of purine biosynthesis. Arrows indicate the action of enzymes. The sites of inhibition by
15 mycophenolic acid (MPA), ribavirin (RI), mizoribine (MI) and aminopterin are marked:

Fig. 2 illustrates the structure and expression of the double labeled GFP plasmid system.

(A) The pIS integrating sphGFP vector. (B) The HGPRT-tpzGFP survival
20 plasmid. P-CMV, P-TK and P-RSV indicate the promoters of herpes TK1, CMV and RSV, respectively. IVS represents the rabbit β globin second intron. PA stands for polyadenylation signal. Filled-in arrows indicate open reading frames translated in the transduced human cells. For construction details, see the Methods section.

25 **Fig. 3** shows photographs and fluorescent images of vector transfected cells.

(C-E) HIS4 cells expressing the pIS construct. (F-H) Clone 12 cells that express both the sphGFP from the pIS construct, and tpzGFP from the

episomal survival plasmid. Panels C and F are photographs of the phase image. Fluorescent images in panels D, E, F and G were obtained using filter sets that preferentially detect sphGFP (D, G), or tpzGFP (E, H). The Clone 12 cells were maintained in hygromycin B selection to retain the survival plasmid. Microscopic images were captured using an Olympus BX40 microscope with a Sony CCD-Iris color video camera. SphGFP was visualized using a filter block with an excitation bandpass of 340-380 nm. TpzGFP was visualized using a filter block with an excitation bandpass of 450-490 nm.

Fig. 4 shows spontaneous loss of tpzGFP-marked survival plasmid in Clone 12 cells.

Cells were maintained in 96 well plates over the entire time period (\square), or grown by continuous passaging in 90 mm petri dishes (Δ). Passaged cells were trypsinized and seeded into microplates on the day of reading. Plates were read using a microplate fluorescence reader (see Methods section). Data points show the mean relative fluorescence ratio between tpzGFP and sphGFP, expressed as a percentage of the same ratio measured from cells maintained under hygromycin B selection. All data represent the mean of fluorescence reading from at least 3 wells.

Figs. 5 & 6 shows that synthetic lethality imposed by MPA causes retention of the survival plasmid.

Fig. 5: Cells were maintained in 96 well microplates, hygromycin B was removed and replaced with GATA medium + MPA in serial dilutions starting with 25 $\mu\text{g/ml}$. Microplates were read after two weeks.

Fig. 6: Cells in 96 well microplates were maintained over the entire time period in either GATA medium + 12.5 $\mu\text{g/ml}$ MPA (\square) or in GATA medium alone (Δ).

Plate reading and data representation is as in Figure 4.

Fig. 7 illustrates the structure of the episomal GSE library plasmid.

Fig. 8 shows two primary transformants of Clone 12 cells transfected with an APRT GSE library examined for retention over time of the tpzGFP fluorescence and its dependency on selection (zeocin resistance) for the GSE vector. 6D6 cells apparently contain a GSE, while 3A6 cells do not.

5 Fig. 9 shows FACS-mediated enrichment for tpzGFP-expressing cells under conditions of synthetic lethality imposed by a GSE library for human GMP synthetase and IMP dehydrogenase (IMPDH). Clone 12 cells held continuously under hygromycin B selection for retention of the survival plasmid (A), without hygromycin B selection (B), or Clone 12 cells
10 transfected by a human GMP synthetase and IMPDH GSE library while in G418 plus 15 μ M G (C) were sorted by FACS six weeks after transfection.

Fig. 10 shows chemical synthetic lethality induced by nucleoside analog inhibitors of IMPDH. Clone 12 cells were grown in microplates in the presence of mizoribine (A), or ribavirin (B), for a period of three weeks
15 before measurement of fluorescent ratio. Values for the fluorescent ratios are shown on the left. Rows A-H, in each matrix, represent the inhibitory drug data. Guanine was at 400 μ M in column 1 and serial dilutions were in the indicated direction. In (A), mizoribine was at 400 μ g/ml in row A and serial dilutions were in the indicated direction. In (B), ribavirin was at 200 μ g/ml in
20 row A and serial dilutions were in the indicated direction.

Fig. 11 shows the detection of chemical synthetic lethality in a blind large-scale test. Clone 12 cells were seeded into 1200 wells in 96 well microplates. Five chemicals were randomly added to three wells each; hygromycin B (H) at 200 μ g/ml, MPA (MP) at 25 μ g/ml, ribavirin (RI) at
25 50 μ g/ml, mizoribine (MI) at 200 μ g/ml and alanosine at 10 μ g/ml. MPA was added in the presence of 200 μ M guanine, ribavirin and mizoribine in 12.5 μ M guanine, while alanosine was added together with 60 μ M adenine.

Plates were read after 28 days and fluorescent ratios are displayed as in Fig. 5.
False positive wells (F) are also labeled.

DETAILED DESCRIPTION OF A PREFERRED EMBODIMENT

Materials and methods

A. **Construction of plasmids.** The plasmid pIS was constructed by replacing the *Bam*HI fragment encoding CD20 from pCMV-CD20 (kind gift
5 from S. van den Heuvel and E. Harlow) with a blunt-ended *Hind*III-*Bam*HI fragment containing the coding sequence of sphGFP from the pGFPsph-b [R] vector (Packard Instruments).

The episomal HGPRT-tpzGFP survival plasmid was constructed by first cloning a *Hind*III-*Bam*HI blunt-ended fragment encoding the tpzGFP and
10 polyadenylation signal from the pGFPtpz-b [R] vector (Packard Instruments) into the *Hind*III site of pCEP4 (Invitrogen). The coding sequence of HGPRT was cloned into pcDNA3 (Invitrogen) and subsequently removed together with the CMV promoter by digestion with *Bgl*II and *Bam*HI. This fragment
15 survival plasmid was produced by cloning the *Kpn*I-*Bam*HI fragment of the pCEP4-HGPRT-tpzGFP vector into the *Kpn*I-*Bam*HI site of pREP4 (Invitrogen), such that tpzGFP is under the influence of the RSV promoter.

B. **Construction of monogenic GSE libraries**

The human adenosine phosphoribosyltransferase (APRT) cDNA, the
20 human GMP synthetase cDNA and the human IMPDH type II cDNA were each amplified by PCR from a human lymphocyte cDNA library. The design of the primers was based on the known cDNA sequence for each. Following amplification, the corresponding PCR segments were isolated, cloned into a KS⁺ plasmid, and their identity verified by DNA sequencing. The human
25 APRT cDNA and, independently, the human GMP synthetase cDNA and the human IMPDH type II cDNA, were digested by partial DNase cleavage into fragments of one hundred to several hundred base pairs. The resulting DNA ends were flushed by Klenow/T4 DNA polymerase and ligated to two DNA

adaptors: one carrying three initiator ATG codons and a *HindIII* recognition sequence, and the other three stop codons and a *XhoI* restriction site. Both codons were designed to be in all three reading frames. The GSE mixture was amplified by PCR with two of the four primers constituting the adaptors, and
5 digested by *HindIII* and *XhoI*. These GSE libraries were then cloned into a pREP9-based episomal vector carrying either the zeocin - or puromycin-resistance genes.

In order to attain a library plasmid encoding zeocin resistance, the zeocin^R coding region together with the bacterial EM-7 promoter were
10 removed from the pVgRXR vector (Invitrogen) by digestion with *PstI* and *Sall*. This fragment was blunted with T4 DNA polymerase and ligated to a T4 DNA polymerase blunted pREP9 vector (Invitrogen) digested with *RsrII* and *BglIII*, creating pREP9zeo. Replacement of the pREP9 neomycin^R coding region with a puromycin^R coding region was carried out as follows. The
15 appropriate fragment from pBSpac was isolated by digesting with *HindIII* and *BamHI* followed by blunting with T4 DNA polymerase. This fragment was cloned into pFastBac HTb (Life Technologies) in the *EheI* site. Following this step, the fragment was removed with *RsrII* and *BamHI* and subcloned into pREP9 digested with *RsrII* and *BglIII*, creating pREP9puro. The *HindIII*
20 and *XhoI* digested library fragments were then cloned into the *HindIII* and *XhoI* sites located in the multiple cloning site of pREP9zeo or pREP9puro.

C. Expression of constructs in cells.

HGPRT-deficient HT1080 fibrosarcoma cells (W.F. Benedict, *et al.*, Cancer Res. 44,3471 (1984)) were maintained in Dulbecco's modified Eagle
25 medium (DMEM) supplemented with 10% fetal calf serum (FCS) and 4mM L-glutamine. This cell line has a generation time of about 24 hours, and a pseudo diploid chromosomal karyotype. Transfections were carried out using the calcium phosphate precipitation technique as previously described (T. Teitz *et al.*, *Proc. Natl. Acad. Sci. USA* 84, 8801 (1987)).

For pIS, selection in G418 (Calbiochem) was carried out at 400 µg/ml, while maintenance was at 50 µg/ml. For the HGPRT-tpzGFP survival plasmid, selection in hygromycin B (Sigma) was at 150 µg/ml while maintenance was at 50 µg/ml. Selection and maintenance of the survival
5 plasmid was also carried out in HAT medium (100 µM hypoxanthine, 0.4 µM aminopterin, 16 µM thymidine; Littlefield, J.W. *Science* **145**, 709 (1964)). GATA medium was DMEM with 10% dialyzed FCS, plus 3.5 µM guanine-HCl, 0.4 µM aminopterin, 16 µM thymidine and 35 µM adenine.

HATA medium was HAT medium plus 60 µM adenine. Concentrations
10 of adenine were determined empirically by plating Clone 12 cells into 96 well microplates in either HAT or GAT medium with varying concentrations of adenine. Loss of survival plasmid was followed on a microplate fluorescence reader and the concentration that was not toxic and allowed a rate of plasmid loss similar to spontaneous rates was chosen.

15 Induction of synthetic lethality in Clone 12 cells using GSE libraries was carried out as follows. The appropriate library in either pREP9zeo or pREP9puro was transfected into cells on 35 mm plates using Lipofectamine Plus (Life Technologies) according to manufacturer's instructions. Cells were trypsinized after 48 hours and seeded into 96 well microplates at a
20 predetermined amount such that one colony or less would be established per well. In our hands, 1 µg of DNA gave 4000 colonies per 35 mm plate of 80% confluent cells. Seeding was in DMEM with 10^4 non-transfected HT1080 cells per well. The appropriate selective drug in either HATA or GATA was added after another 24 hours. Selection for the libraries was at 750 µg/ml
25 zeocin for pREP9zeo or 0.5 µg/ml puromycin for pREP9puro. Maintenance was at 400 µg/ml zeocin or 0.2 µg/ml puromycin, respectively.

D. Fluorescent scanning of microtiter plates.

For fluorescent scanning, cells were trypsinized and distributed at 30,000 cells/well into 96 well microplates (TPP). Growth medium was changed twice a week and plates were grown for up to 75 days. Although cell populations were very dynamic due to shedding of large clumps, almost all wells contained viable, growing cells for the entire span of the experiment. Plates were prepared for scanning by replacement of medium in wells with Hank's balanced salt solution without phenol red. This procedure minimized background fluorescence from the growth medium while maintaining maximal viability. Plates were scanned with an FL600 microplate fluorescence reader using the KC4 software (Biotek Instruments). Excitation for sphGFP was at 380nm with a bandpass of 20nm, while emission was measured at 508nm with a bandpass of 40nm. Excitation of tpzGFP was at 495nm with a bandpass of 20nm, while emission was measured at 535nm with a bandpass of 40nm. To avoid possible artifacts, all wells within a given experiment were assayed for the fluorescence of the two GFP mutants using fixed sensitivities.

Integrated sphGFP was used as an internal control for the number of cells. This was achieved by dividing the relative fluorescence resulting from the episomal tpzGFP vector by the relative fluorescence for sphGFP for each well. This ratio was then divided by the average fluorescence ratio for cells maintained under hygromycin B or HAT selection, resulting in a value representing percent remaining fluorescence for each well as compared to wells maintained under continuous selection. The data points are an average for all wells and the calculated standard deviation. Cells were returned to growth medium immediately following scanning.

E. FACS enrichment for tpzGFP expressing cells

Cells transfected with the GMP synthetase and IMPDH GSE library were continuously grown in 15 μ M guanine (G) plus 400 μ g/ml zeocin in 100 mm plates and the population was expanded.. Expression of tpzGFP was

followed during this time period by trypsinizing cells, several washes in PBS, resuspension in Hank's balanced salt solution and analysis of fluorescence on a FACSort (Becton Dickinson) using a 488 nm laser. After a period of six weeks following transfection, 2% of the cells retained high levels of tpzGFP, while the remaining cells lost most of their fluorescence. The highly fluorescent cells were sorted and reseeded at one cell or less per well into 96 well microplates together with 10^4 non-transfected HT1080 cells. When colonies became apparent, microplates were read on a microplate fluorescence reader.

Alternatively, the highly fluorescent FACS-sorted cells can be extracted for low-molecular-weight DNA present in the Hirt supernatant. Cleavage of the plasmid DNAs with the *NotI* restriction endonuclease and calf intestine phosphatase treatment, excludes the survival plasmid from plasmid DNAs amplified through bacterial transformation to β -lactamase (Amp) resistance. Plasmid DNAs recovered from these bacteria is transfected as a pool to clone 12 cells in order to generate secondaries held under guanine (G) and zeocin selection. Following a six weeks shedding period the fluorescent cells are FACS sorted, and either reseeded as single cells into microplate wells, as outlined above, or the putative GSE-containing plasmids are recovered via Hirt supernatant extraction, *NotI* digestion and bacterial transformation. Verification of GSE activity entails transfection of GSE-plasmid into cells, followed by demonstration of tpzGFP fluorescence-retention coupled to decreased IMPDH- or GMP synthetase-activity (conversion of IMP to XMP or XMP to GMP, respectively).

EXAMPLES

I. Establishment of a model system

In order to develop a synthetic lethality screening method in human cells, Epstein-Barr virus (EBV) based episomal vectors, which can replicate autonomously as a low copy number episome in human cells of diverse tissues, were selected as the basis for the survival plasmid (J.L. Yates, N. Warren and B. Sugden, *Nature* 313, 812 (1985); U.S. Patent No. 4,686,186, whose contents are incorporated herein). However, this vector is an imperfect episome because its retention in human cells requires continued selection for a dominant selectable marker gene built into the vector (D. Reisman, J. Yates and B. Sugden, *Mol. Cell. Biol.* 5, 1822 (1985). M.P. Calos, *Trends Genetics* 12, 463 (1996)). In the design of the system for human cells, advantage was taken of this spontaneous gradual plasmid loss, by creating synthetic lethal conditions under which retention of the episomal plasmid is essential for viability.

As a model system for the establishment of the method, the biosynthetic pathway leading to the production of guanosine monophosphate (GMP) was chosen (Fig. 1). This pathway has been thoroughly studied biochemically and is particularly amenable to a synthetic lethality screen. First of all, the gene of interest in the model system, hypoxanthine-guanine phosphoribosyltransferase (HGPRT), is non-essential for cell survival, since it works in salvage pathways by converting hypoxanthine and guanine to IMP and GMP, respectively. Secondly, immortalized HGPRT-deficient human cell lines are available. Also, a major advantage of this model system is that *de novo* GMP synthesis can be specifically blocked by certain chemical reagents (Fig. 1). Accordingly, the HGPRT deficient human cells should become dependent on the HGPRT expressing "survival plasmid", when the *de novo* pathway is blocked by aminopterin or mycophenolic acid (MPA), in the

presence of the HGPRT precursors hypoxanthine and guanine, respectively (Littlefield, *op.cit.*).

II. Stable transfection of an internal control fluorescent marker

In order to establish synthetic lethality as a high throughput screening
5 system based on fluorescent readout, it is essential to have an internal
fluorescent reporter which normalizes the fluorescent reading from the
episomal survival plasmid, relative to cell number. To this end, the
sapphire-blue green fluorescent protein (sphGFP), a mutant form of the
natural GFP from the jellyfish *Aequara victoria*, was chosen (U.S. Patent No.
10 5,625,048, the contents of which are incorporated herein). The sphGFP
coding region was cloned into a transcription unit driven by the strong CMV
immediate-early promoter (U.S. Patent No. 5,168,062, the contents of which
are incorporated herein), and situated upstream of a neo^R transcription unit,
thus creating the vector pIS (Fig. 2a). As a recipient cell line the
15 HGPRT-deficient variant of the HT1080 fibrosarcoma cell line was chosen
(W.F. Benedict, B.E. Weissman, C. Mark and E.J. Stanbridge, Cancer Res. 44,
3471 (1984)).

The pIS vector was transfected into these cells, stable clones were
selected in G418, and examined with a fluorescent microscope. Clones with
20 >99% fluorescing cells were chosen for further examination (Fig. 3). These
were seeded into 96-well microplates, and scanned for fluorescence intensity
using a microplate fluorescent reader, as described in the Methods section.
Compared to the recipient cells, or medium alone, up to 38-fold fluorescence
enhancement was recorded for the sphGFP transformants (data not shown).
25 As expected, in the linear range of sphGFP reading, a close correlation was
seen between the number of cells and the fluorescent intensity. The
fluorescent intensity of these cells did not vary appreciably when removed
from continuous G418 selection. Thus, the fluorescence levels obtained from

the stably integrated sphGFP mutant gene are appreciable and can be easily detected as a mass population by a fluorescent microplate reader.

III. Generation of stable transfectants harboring the episomal survival plasmid

5 Survival plasmids containing a transcription unit for the human HGPRT cDNA (gene of interest) and a second GFP mutant gene, were constructed onto the backbone of the EBV-based pCEP4/pREP4 episomal vectors (Fig. 2b), as described in the Methods section. These vectors replicate autonomously as episomes in human cells due to the EBV-*oriP* and EBNA-1
10 elements (J.L. Yates, N. Warren and B. Sugden, *Nature* **313**, 812 (1985)). They also contain the hygromycin phosphotransferase dominant selectable marker, the bacterial *colE1* origin of DNA replication and the β lactamase gene.

In order to identify the survival plasmid, a second GFP variant was
15 incorporated, the topaz-green GFP mutant gene (tpzGFP), whose expression can be distinguished from the sphGFP mutant. TpzGFP has an excitation peak (514nm) which does not overlap with that of sphGFP (395nm), allowing for double-label fluorescence measurements. The corresponding emission peaks are 527nm for tpzGFP and 511nm for sphGFP. TpzGFP was cloned under the
20 influence of the RSV promoter (Fig. 2b). The human HGPRT cDNA was inserted in between the unique restriction sites *HindIII* and *BamHI*, so that it can be easily replaced by any human cDNA of interest (Fig. 2b). This construct, a HGPRT-tpzGFP survival plasmid, was introduced into one cell clone, HIS4, which displayed stable expression of the integrated sphGFP
25 reporter. Stable clones resistant to hygromycin B were selected for further study, as described in the Methods section.

Most hygromycin B resistant clones were also resistant to HAT medium, indicating expression of the HGPRT transcription unit. Scanning by fluorescence microscopy was used to select several clones that express the

tpzGFP in >99% of their cells. The fluorescence resulting from these two GFP variants, one stably integrated into the genome (sphGFP) and one episomal (tpzGFP), could be distinguished by use of two different filter blocks (Fig. 3, D and G vs. E and H). Similar numbers of these cells were
5 then plated into 96 well microplates and scanned by a fluorescent microplate reader. This scanning revealed up to a 140-fold tpzGFP fluorescence increase over HIS4 autofluorescence (data not shown). It can therefore be concluded that the double-label fluorescence from the sphGFP and tpzGFP can be readily distinguished at both the single cell level by fluorescence microscopy,
10 as well as at the mass culture level when grown in microplates, by a fluorescence microplate reader.

IV. Spontaneous loss of the survival plasmid

It was next determined whether spontaneous loss of the survival plasmid could be detected by fluorescence measurements. It was imperative to
15 show that in microtiter plates the expected plasmid loss occurs and could be detected. This is because an inherent feature of the proposed high throughput method is that scanning for genes or chemical reagents, that are synthetically lethal with a human gene of interest, will be performed on cell clones grown in microplate wells. The dynamics of cell division, and therefore the rate of
20 the survival plasmid loss, could be very different in cells grown for long periods in microplates, as opposed to cells stimulated to divide by a regimen of periodic trypsinization, dilution and reseeded. Accordingly, measurement of fluorescence after removal of drug selection was carried out in cells continuously passaged in 90 mm plates as well as in cells grown in microtiter
25 plates.

Results from one isolate, Clone 12, carrying an integrated sphGFP gene and an episome-encoded tpzGFP are shown in Fig. 4. Following removal of hygromycin B from the medium, the tpzGFP and sphGFP fluorescence ratios were monitored over time. The calculated ratio was

normalized to readings taken at the same time point from cells kept continuously under hygromycin B selection. As shown in Fig. 4, fluorescence from the survival plasmid marked with tpzGFP decayed rather quickly, so that after about one month, Clone 12 lost 80-90% of its initial fluorescence. 5 Importantly, no significant difference in the rate of fluorescence decay could be detected between the cells maintained in microplate wells as opposed to those maintained by continuous passaging in petri dishes (Fig. 4). Assuming that one of the major factors affecting EBV-based plasmid loss is the rate of cell division, it could be that besides the multilayer growth of these 10 transformed cells, the cell shedding which was observed in the microplate wells may also contribute to the dynamics of cell division.

To test whether the gradual loss of tpzGFP fluorescence over time indeed reflects the loss of survival plasmid, two assays were conducted. In one, low molecular weight DNA present in Hirt supernatants (B. Hirt, *J. Mol.* 15 *Biol.* 26, 365 (1967) of Clone 12 cells was collected at various times after removal from hygromycin B selection. This DNA was used for bacterial transformation. It was found that the decrease of AmpR colonies correlated well with the loss of tpzGFP fluorescence over time (Table 1). In the second assay, a plasmid segregation assay (D. Reisman, J. Yates and B. Sugden, *Mol.* 20 *Cell. Biol.* 5, 1822 (1985) was carried out. At each time point after drug removal, cells were reseeded into petri dishes containing hygromycin B. It was found that the number of colonies able to grow in the presence of hygromycin B, did indeed decrease at later time points (data not shown).

Table 1

Monitoring of spontaneous survival plasmid loss by Hirt supernatant mediated bacterial transformation.

Clone 12 cells were plated at the beginning of the experiment in DMEM without hygromycin B. Cells were continuously passaged throughout the entire experiment. Low-molecular weight DNA present in Hirt supernatants was collected at the indicated time points. All Hirt supernatants were normalized by addition of 1 ng of a chloramphenicol-resistant plasmid prior to the beginning of cell extraction. Each Hirt supernatant transformation of bacteria was plated both on chloramphenicol and ampicillin plates. Values in table were normalized to the number of colonies counted on the chloramphenicol plates.

Days without selection	Bacterial transformants per 10 ⁶ Clone 12 cells	Plasmid loss (k) per day (%) *
0	628	
21	38	13.4
25	23	13.2
38	16	9.7
46	0	

* Calculated according to $2.303 \log (N_0/N) = kT$, where N_0 = % Amp^R colonies at time zero (100%), N = % Amp^R colonies remaining after propagation for T days without hygromycin B selection and k = % loss of plasmid per day.

V. Detection of chemical reagent induced synthetic lethality

These results demonstrated that, in the absence of selection, the HGPRT-tpzGFP survival plasmid is unstable in HGPRT-deficient HT1080 cells. Its loss or retention can be determined by measuring its normalized fluorescence in a microplate reader. It was then necessary to test whether these features would enable the tracing of a synthetic lethality condition.

The biosynthesis of GMP from IMP via XMP can be efficiently blocked using MPA, which inhibits IMP dehydrogenase (Fig. 1). Under these conditions, normal HGPRT-positive cells can use supplied guanine to produce GMP via the salvage pathway, and survive, while HGPRT-deficient cells die.

5 Clone 12, as an inherently HGPRT-deficient cell line, must retain the HGPRT-tpzGFP survival plasmid in order to remain alive in this synthetic lethality situation. Indeed, when hygromycin B was removed from Clone 12 cells grown in GATA medium (medium supplemented with guanine, aminopterin, thymidine and adenine – see Methods section), spontaneous loss

10 over time of the survival plasmid occurred, as traced by a decrease in tpzGFP fluorescence (Fig. 6).

It has been shown that under the specific conditions used, this loss is enabled due to a relative surplus of adenine, which besides serving as a precursor for AMP biosynthesis, allows GMP to be synthesized via the

15 AMP-IMP-XMP pathway (data not shown, and see also Methods and Fig. 1). In contrast, addition of MPA to the GATA medium at successively higher concentrations, caused increasing retention of the survival plasmid, which could be detected by an increase in tpzGFP to sphGFP fluorescence ratio. A dose response was observed which reached a plateau at fluorescence levels

20 similar to those obtained when HAT selection is imposed (Fig. 5). Moreover, as shown in Fig. 6, when fluorescence was observed over time, MPA could cause retention of the survival plasmid for the entire time period, while cells without MPA continued to lose tpzGFP fluorescence. Importantly, almost identical patterns of decay or retention in the presence of MPA were found

25 when cells were grown in medium plus 3 μ M guanine, without aminopterin or adenine (data not shown).

IMP dehydrogenase (IMPDH) has two isoforms and is considered to be the rate-limiting enzyme in guanine nucleotide biosynthesis. Two basic types of drugs can effectively inhibit the enzyme: nucleoside analogs and non-

nucleoside inhibitors. MPA is of the second class and binds the NAD site within the enzyme. Nucleoside analog inhibitors bind to the IMP substrate site. Accordingly, it was asked whether one could detect synthetic lethality when nucleoside analog inhibitors were applied to Clone 12 cells. We chose
5 for this assay two drugs, ribavirin and mizoribine, both in use against viral infections. We tested both drugs on Clone 12 cells grown in 96 well microtiter plates in serial dilutions of the drugs as well as serial dilutions of guanine. The observed matrices of results are shown in Fig. 10. Both drugs caused retention of the survival plasmid, in a way that was dependent on the concentration of
10 each drug as well as that of guanine. These matrices allowed sensitive measurement of the synthetic lethal effects imposed by these nucleoside analogs.

Next, we tested if the synthetic lethality assay could be used in a blind test to screen for these IMPDH inhibitors. Clone 12 was seeded into 1200
15 wells in microtiter plates in medium lacking selection. MPA, ribavirin, mizoribine, and hygromycin B were added at random (together with guanine) to three wells. Alanosine, an inhibitor of adenylosuccinate synthase (an enzyme in the pathway converting IMP to AMP) was also added as a negative control. As expected, the survival plasmid was not retained in the presence of
20 alanosine (data not shown). However, the presence of all three IMPDH inhibitors and hygromycin B was clearly detected as were two wells containing false positive cells (Fig. 11). The calculated false positive rate for this experiment was 1/600 and was similar to previous control experiments (data not shown).

25 These results demonstrate the feasibility of a synthetic lethality screen in cultured human cells, using a sensitive fluorescent assay allowing detection of synthetic lethality imposed with a chemical reagent.

VI Detection of synthetic lethality imposed by human APRT and GMP synthetase – GSE libraries

In order to genetically disrupt the activity of human genes in a random fashion, and then use the synthetic lethality screen to identify those genes which are synthetically lethal with the gene of interest, the GSE methodology was employed (L.P. Deiss and A. Kimchi, *Science* **252**, 117 (1991); A.V. Gudkov *et al.*, *Proc. Natl. Acad. Sci., U.S.A.* **90**, 3231 (1993); V.S. Ossovskaya *et al.*, *Proc. Natl. Acad. Sci., U.S.A.* **93**, 10309 (1996)). The essence of this method is the generation of short truncated cDNAs or antisense cDNAs whose expression acts, at a variable frequency, in a dominant negative fashion within the transfected host cells. For this purpose pREP9-based human episomal vectors have been constructed carrying a unique dominant selectable marker, zeocin or puromycin resistance genes (Fig. 7).

An APRT GSE library incorporated into a zeocin-resistance containing episomal vector (see Methods for construction details) was transfected into Clone 12 cells held under selection for retention of the survival plasmid (hygromycin B resistance).

Following a three days expression period, the transfected cells were trypsinized off the petri dishes and seeded onto microplates at an estimated cell density of one transformant or less per well. The hygromycin B in the medium was replaced by zeocin in HATA medium. Zeocin selection ensures the retention of the GSE library in Clone 12 cells. Deficiency of the endogenous HGPRT gene dictates that in HAT medium, survival of Clone 12 cells is dependent on HGPRT-mediated conversion of hypoxanthine to IMP, with the HGPRT being encoded by the survival plasmid. Addition of 60 μ M adenine to HAT (HATA medium) diverts the synthesis of GMP as well as AMP from the HGPRT-dependent salvage pathway, to the APRT-mediated conversion of adenine to AMP followed by the IMP-XMP-GMP pathway.

This diversion results in the spontaneous loss of the survival plasmid in Clone 12 cells (see Methods section). However, incapacitation of APRT activity by a GSE should result in retention of the survival plasmid, because its HGPRT-encoded activity becomes essential for viability. The GSE library
5 transfected Clone 12 cells were read periodically while in microplates, for the tpzGFP to sphGFP double-label fluorescence ratio using a microplate fluorescence reader. After about 6-8 weeks a small number of wells retained a high tpzGFP to sphGFP fluorescence ratio, meaning retention of the survival plasmid.

10 If retention of the survival plasmid had occurred due to incapacitation of APRT enzyme activity (as opposed for example to integration of the episomal survival plasmid into the cell genome, making it immobile), then it must be dependent on the GSE-containing plasmid. The dependence of tpzGFP fluorescence on selection to zeocine resistance encoded by the GSE
15 vector plasmid was therefore tested. Removal of zeocine selection in clone 6D6 resulted in a typical decrease of tpzGFP fluorescence. In contrast, primary transformant 3A6 did not exhibit retention of the survival plasmid even in the presence of zeocin (Fig. 8). Thus, primary transformant 6D6 is likely to contain an APRT GSE.

20 In order to rescue the GSE-containing episome, low-molecular weight DNA present in the Hirt supernatant fraction of fluorescing cell clones was transformed into *E. coli* while selecting for zeocin resistance. Structural characterization of the plasmid clones recovered from the human cell transformants revealed on the average one to four different plasmids (that is to
25 say different inserts). To determine which of these plasmids encoded an actual GSE, individual plasmids were reintroduced into naive Clone 12 cells. Individual secondary transformant clones were tested for retention of tpzGFP fluorescence, as outlined above. A few exhibited retention of high tpzGFP fluorescence, indicating synthetic lethality relieved by HGPRT-expression

from the survival plasmid. Additionally, the cDNA inserts present in several candidate GSEs were cloned into an episomal plasmid with a puromycin resistance selectable marker. Secondary transformants were generated and their characterization with respect to tpzGFP fluorescence retention followed the protocol outlined above.

The secondary transformants retaining high tpzGFP fluorescence were further characterized for:

1. dependency on continuous selection for zeocin (or puromycin) resistance. If synthetic lethality was imposed by an APRT GSE, removal of selection for zeocin (or puromycin) which results in loss of the GSE-containing episomal plasmid, should be reflected in decreased tpzGFP fluorescence.
2. conferring of sensitivity to alanosine, which blocks conversion of IMP to AMP and therefore causes dependency on APRT-mediated conversion of adenine to AMP. Transfectants with reduced APRT activity because of a GSE action, should be more sensitive to alanosine than their parent cells.

Most, if not all, of the highly tpzGFP fluorescing secondary transformants exhibited these features and were considered as putative GSEs. This conclusion may be further strengthened, for example, by carrying out a dose response experiment of tpzGFP fluorescence versus zeocin/puromycin concentration.

The recovered plasmids may then be analyzed for the DNA sequences which make up the GSE inserts, in order to characterize the polarity, truncated sense or antisense cDNA, as well as location within the APRT cDNA.

In a further example, the method of the invention may be utilized with respect to human GMP synthetase and IMPDH, albeit with one major difference. Instead of seeding GSE library transfected cells into microtiter plates soon after transfection, the cells are maintained in large petri dishes or

spinner flasks for non-adherent cells for six weeks in G plus zeocin medium. They were then analyzed by FACS in comparison to Clone 12 cells maintained constitutively under hygromycin B selection or without selection. As shown in Fig. 9A, the majority (75%) of Clone 12 cells held under
5 hygromycin B selection exhibit high fluorescence due to retention of tpzGFP encoding survival plasmids. In contrast, Clone 12 cells left without selection or transfected by the human GMP synthetase and IMPDH GSE library and released for six weeks from hygromycin B selective pressure, exhibited 0.2% and 2% of cells with high tpzGFP fluorescence (Figs. 9B and 9C,
10 respectively).

The latter population was sorted and episomal DNAs containing GMP synthetase or IMPDH cDNA fragments were recovered via Hirt supernatant extraction, *NotI* cleavage and bacterial transformation followed by plasmid purification. These plasmid DNAs were transfected for secondaries into
15 Clone 12 cells and several tenths seeded as single transfected cells onto 96 well microplates and scanned periodically for tpzGFP to sphGFP fluorescence ratio as outlined above. The remaining secondaries were subjected to another round of FACS enrichment followed by the generation of tertiary transfectants as outlined. These secondary/tertiary transfectants are considered to harbor
20 putative GMP synthetase/IMPDH GSE/s.

In a manner similar to the monogenic GMP synthetase or IMPDH GSE library described above, whole genome GSE libraries may be scanned for genetically interacting genes. This entails among others, the construction of GSE libraries from, preferably, whole tissue normalized cDNA libraries
25 [M.F. Bonaldo et al., Genome Res., 791 (1996)], as well as several of the FACS enrichment steps outlined above.

The GSE libraries may be prepared from whole embryonal or adult tissue, as well as from particular cell lines. The genes may be expressed under normal or abnormal physiological states, including malignancy. With

respect to mouse or other rodents, the GSE libraries may also be prepared from any of a number of embryonal developmental stages. The source for the GSE library may also be a previously enriched or selected cDNA library. Enrichment/selection may involve solution hybridization or prior selection via
5 DNA chips. Ultimately, GSE libraries may be prepared from a full-length cDNA pool encompassing the complete coding potential of the organism.

High throughput fluorescent scanning of transfected cells which maintain the episomal survival plasmid is expected to reveal novel genes whose GSEs confer synthetic lethality upon the mutated gene of interest.

10 VII Rodent model of synthetic lethality

Autonomous replication of a survival plasmid in rodent cells may be conferred by either the EBV-based pREP/pCEP vectors described above, or by the polyoma virus origin of DNA replication together with the virus segment encoding the large T antigen (Z. Zhu et al., J. Virol. 51, 170 (1984);
15 G. Camenisch et al., Nuc. Acids Res. 24,3707 (1996)).

A DNA segment harboring the wild-type polyoma virus origin of DNA replication or its mutated enhancer PyEC F9-5 M. Vasseur et al., J. Virol., 43, 800 (1982) was ligated to a modified polyoma virus early region encoding the large T antigen only. The latter was excised by *BclI* and *HincII*
20 restriction enzymes from the plasmid PyLT1 [Z. Zhu et al., (1984)], cloned into the versatile plasmid pJRD 184, and subsequently removed via a blunt-ended *SpeI* and *BstEII* cleavage. This segment was inserted in place of the Herpes EBV encoded *oriP* and EBNA-1 gene. This was accomplished by cleavage of the survival plasmid described in Fig. 2b with *XbaI* and *BstEII*
25 restriction enzymes, followed by blunting of the 8 kb long fragment and its ligation to the polyoma derived DNA segment. The resulting survival plasmid or the EBV-based survival plasmid described above may be used in

chemical/genetic screening methods for synthetic lethal-chemicals or -mouse genes as described above with respect to human genes.

CLAIMS:

1. A method for screening a chemical library comprising a plurality of molecule types in mammalian cells having a genome, in order to identify a said molecule type having a gene-specific lethal property in said cell, said genome comprising a gene of interest which carries a non-lethal mutation
5 therein, said method comprising:
 - (a)transfecting a first reporter gene into said cells, and selecting clones stably expressing said reporter gene;
 - (b) introducing into said cells an episome comprising a
10 functioning copy of said gene of interest, a second reporter gene, a dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within said cells, wherein said episome is spontaneously lost from said cells, and growing said cells in the presence of a selection compound which
15 selects for said dominant selectable marker;
 - (c)selecting cell clones stably expressing said second reporter gene and said functioning copy of said gene of interest;
 - (d) seeding of said cells into a plurality of cell chambers and removing said selection compound;
 - 20 (e)adding a said molecule type of said chemical library to each of said plurality of cell chambers, measuring expression of said first and second reporter genes in said chambers, and calculating the ratio of said measured expressions, thereby indicating retention of said episome; and
 - 25 (f) identifying a cell chamber in which said episome is retained, thus identifying a molecule type having a mutant gene-specific lethal property in said cell.
2. A method according to Claim 1, wherein said mammalian cells are human cells.

3. A method according to Claim 1, wherein said mammalian cells are rodent cells.
4. A method according to Claim 1, wherein the products of said reporter genes are fluorescent proteins.
- 5 5. A method according to Claim 4, wherein the product of said first reporter gene has an excitation peak which differs from the excitation peak of the product of said second reporter gene.
6. A method according to Claim 2, wherein said cells are human cancer cells.
- 10 7. A method according to Claim 6, wherein said gene of interest is specifically incapacitated in said human cancer cells.
8. An episomal plasmid compatible with a mammalian cell comprising a functional copy of a gene of interest, a reporter gene, a dominant selectable marker gene, an origin of DNA replication, and a nuclear antigen essential for
15 replication of the episome, said episome being spontaneously lost from said cell,
wherein the product of said reporter gene is a mutant green fluorescent protein (GFP).
9. An episomal plasmid according to Claim 8 wherein said origin of
20 DNA replication is selected from the group consisting of the EBV origin of DNA replication (*oriP*) and the polyoma virus origin of DNA replication, wherein when the origin of DNA replication is EBV, the nuclear antigen is EBNA-1 and when the origin of DNA replication is polyoma virus, the nuclear antigen is large T antigen gene whose promoter may have either a
25 wild-type or a mutated enhancer.
10. A method for screening a chemical library comprising a plurality of molecule types in mammalian cells having a genome, in order to identify a said molecule type having a gene-specific lethal property in said cell, said cell expressing a gene of interest, said method comprising:

(a) stably expressing said reporter gene;

(b) introducing into said cells an episome comprising a dominant-negative mutant of said gene of interest, a second reporter gene, a dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within said cells, wherein said episome is spontaneously lost from said cells, and growing said cells in the presence of a selection compound which selects for said dominant selectable marker;

(c) selecting cell clones stably expressing said second reporter gene and said dominant-negative mutant of said gene of interest;

(d) seeding of said cells into a plurality of cell chambers and removing said selection compound;

(e) adding a said molecule type of said chemical library to each of said plurality of cell chambers, measuring expression of said first and second reporter genes in said chambers, and calculating the ratio of said measured expressions, thereby indicating retention of said episome; and

(f) identifying a cell chamber in which said episome is retained, thus identifying a molecule type having a gene-specific lethal property in said cell.

11. A method according to Claim 10, wherein said mammalian cells are human cells.

12. A method according to Claim 10, wherein said mammalian cells are rodent cells.

13. A method according to Claim 10, wherein the products of said reporter genes are fluorescent proteins.

14. A method according to Claim 13, wherein the product of said first reporter gene has an excitation peak which differs from the excitation peak of the product of said second reporter gene.

15. A method according to Claim 11, wherein said cells are human cancer cells.

16. A method according to Claim 15, wherein said gene of interest is an oncogene specifically overexpressed in said human cancer cells.

5 17. An episomal plasmid compatible with a mammalian cell comprising a dominant-negative mutant of a gene of interest, a reporter gene, a dominant selectable marker gene, an origin of DNA replication and a nuclear antigen essential for replication of the episome, said episome being spontaneously lost from said cell,

10 wherein the product of said reporter gene is a mutant green fluorescent protein (GFP).

18. An episomal plasmid according to Claim 17 wherein said origin of DNA replication is selected from the group consisting of the EBV origin of DNA replication (*oriP*) and the polyoma virus origin of DNA replication,
15 wherein when the origin of DNA replication is EBV, the nuclear antigen is EBNA-1 and when the origin of DNA replication is polyoma virus, the nuclear antigen is large T antigen gene whose promoter may have either a wild-type or a mutated enhancer.

19. A method for screening a collection of DNA molecules selected from
20 the group consisting of antisense cDNA, truncated cDNA, DNA encoding interfering RNA (RNAi), full-length cDNA and genomic DNA, in order to identify among them one or more modulators of gene function which are synergistically lethal to a mammalian cell together with an incapacitated gene of interest, said cell having a genome which comprises said incapacitated
25 gene of interest, said method comprising:

(a) transfecting a first reporter gene into said cell, and selecting clones stably expressing said reporter gene;

(b) introducing into said cells an episome comprising a functioning copy of said gene of interest, a second reporter gene, a

first dominant selectable marker, an origin of DNA replication and a nuclear antigen gene essential for replication of the episome within said cells, wherein said episome is spontaneously lost from said cells, and growing said cells in the presence of a selection compound which selects for said first dominant selectable marker;

(c) selecting cell clones stably expressing said second reporter gene and said functioning copy of said gene of interest;

(d) incorporating each of said DNA molecules into vector vehicles containing a second dominant selectable marker gene;

(e) transfecting said cells with said vector vehicles so that each transfected cell contains on the average approximately one to several of said molecules, and allowing expression of said molecules in said cells;

(f) seeding said transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, and initiating conditions for selection of said second dominant marker, while removing said selection compound for said first dominant selectable marker;

(g) measuring expression of said first and second reporter genes in said chambers, and calculating the ratio of said measured expressions, thereby indicating retention of said episome; and

(h) identifying a cell chamber in which said episome is retained, thus identifying a DNA molecule which is a said modulator of gene function.

20. A method according to Claim 19, wherein instead of step (f), the transfected cells of step (e) are subject to:

(a) removal of selection for said first dominant selectable marker, and thus resulting in survival plasmid loss;

(b) continuous selection for the expression of said second dominant selectable marker as a pool of transfectants;

(c) sorting by Fluorescent Activated Cell Sorter (FACS) for those cells retaining expression of the second reporter gene encoded by the survival plasmid; and, either directly or after additional FACS enrichment steps involving generation of secondary/tertiary transformants,

(d) seeding said FACS sorted transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, while continuing selection for the expression of said second dominant marker.

21. A method according to Claim 19, wherein said vector vehicles in step (d) is selected from the group consisting of an episomal mammalian expression vector, a retroviral vector, an episomal viral vector, and a chimeric transposable element.

22. A method according to Claim 19, wherein said mammalian cells are human cells.

23. A method according to Claim 22 wherein the episome of step 1(b) of Claim 1 carries the EBV origin of DNA replication (*oriP*) and the EBNA-1 nuclear antigen.

24. A method according to Claim 19, wherein said mammalian cells are mouse embryo fibroblasts.

25. A method according to Claim 24 wherein the episome of step 1(b) of Claim 1 carries either the EBV-origin (*oriP*) and the EBNA-1 nuclear antigen, or the polyoma virus origin of DNA replication and the polyoma virus large T antigen gene which comprises the polyoma promoter, and the polyoma promoter has either a wild type or a mutated enhancer.

26. A method according to Claim 19, wherein the products of said reporter genes are fluorescent proteins.

27. A method according to Claim 26, wherein the product of said first reporter gene has an excitation peak which differs from the excitation peak of the product of said second reporter gene allowing for double-label fluorescent reading within the same cell.
- 5 28. A method according to Claim 22, wherein said cells are human cancer cells.
29. A method according to Claim 28, wherein said gene of interest is a gene specifically defective in said human cancer cells.
30. A method for screening a collection of DNA molecules selected from
10 the group consisting of antisense cDNA, truncated cDNA, DNA encoding RNAi, full-length cDNA and genomic DNA, in order to identify among them one or more modulators of gene function which are synergistically lethal to a mammalian cell, said cell having a genome which expresses a gene of interest, said method comprising:
- 15 (a)transfecting a first reporter gene into said cell, and selecting clones stably expressing said reporter gene;
- (b) introducing into said cells an episome comprising a dominant-negative mutant of said gene of interest, a second reporter gene, a first dominant selectable marker, an origin of DNA replication
20 and a nuclear antigen gene essential for replication of the episome within said cells, wherein said episome is spontaneously lost from said cells, and growing said cells in the presence of a selection compound which selects for said first dominant selectable marker;
- (c)selecting cell clones stably expressing said second reporter
25 gene and said dominant-negative mutant of said gene of interest;
- (d) incorporating each of said DNA molecules into vector vehicles containing a second dominant selectable marker gene;
- (e)transfecting said cells with said vector vehicles so that each transfected cell contains on the average approximately one to several

of said molecules, and allowing expression of said molecules in said cells;

(f) seeding said transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, and initiating conditions for selection of said second dominant marker, while removing said selection compound for said first dominant selectable marker;

(g) measuring expression of said first and second reporter genes in said chambers, and calculating the ratio of said measured expressions, thereby indicating retention of said episome; and

(h) identifying a cell chamber in which said episome is retained, thus identifying a DNA molecule which is a modulator of gene function.

31. A method according to Claim 30, wherein instead of step (f), the transfected cells of step (e) are subject to:

(a) removal of selection for said first dominant selectable marker, and thus resulting in survival plasmid loss;

(b) continuous selection for the expression of said second dominant selectable marker as a pool of transfectants;

(c) sorting by Fluorescent Activated Cell Sorter (FACS) for those cells retaining expression of the second reporter gene encoded by the survival plasmid; and either directly or after additional FACS enrichment steps involving generation of secondary/tertiary transformants,

(d) seeding said FACS sorted transfected cells into a plurality of cell chambers under conditions of one stably transfected cell or less per chamber, while continuing selection for the expression of said second dominant marker.

32. A method according to Claim 30, wherein said vector vehicles in step (d) is selected from the group consisting of an episomal mammalian expression vector, a retroviral vector, a viral vector, and a chimeric transposable element.
- 5 33. A method according to Claim 30, wherein said mammalian cells are human cells.
34. A method according to Claim 33 wherein the episome of step 10(b) carries the EBV origin of DNA replication (*oriP*) and the EBNA-1 nuclear antigen.
- 10 35. A method according to Claim 30, wherein said mammalian cells are mouse embryo fibroblasts.
36. A method according to Claim 35 wherein the episome of step 10(b) of Claim 10 carries either the EBV-origin (*oriP*) and the EBNA-1 nuclear antigen, or the polyoma virus origin of DNA replication and the polyoma virus large T antigen gene which comprises the polyoma promoter, and the polyoma promoter has either a wild type or a mutated enhancer.
- 15 37. A method according to Claim 30, wherein the products of said reporter genes are fluorescent proteins.
38. A method according to Claim 37, wherein the product of said first reporter gene has an excitation peak which differs from the excitation peak of the product of said second reporter gene allowing for double-label fluorescent reading within the same cell.
- 20 39. A method according to Claim 33, wherein said cells are human cancer cells.
- 25 40. A method according to Claim 39, wherein said gene of interest is an oncogene specifically overexpressed in said human cancer cells.
41. A kit for screening a chemical library comprising a plurality of molecule types in mammalian cells having a genome, in order to identify a said molecule having a gene-specific lethal property in said cell, comprising:

(a) an integration plasmid comprising a first reporter gene; and

(b) an episomal plasmid compatible with a mammalian cell comprising a functional copy of a gene of interest or a dominant-negative mutant of a gene of interest, a reporter gene, a dominant selectable marker gene, an origin of DNA replication and a nuclear antigen essential for replication of the episome, said episome being spontaneously lost from said cell.

42. A kit according to Claim 41 wherein said molecule types are drug compounds.

43. A kit for screening a group of DNA molecules in order to identify among them one or more modulators of gene expression which are synergistically lethal to a mammalian cell together with a gene of interest, comprising:

(a) an integration plasmid comprising a first reporter gene;

(b) an episomal plasmid compatible with a mammalian cell comprising a functional copy of a gene of interest or a dominant-negative mutant of a gene of interest, a reporter gene, a dominant selectable marker gene, an origin of DNA replication and a nuclear antigen essential for replication of the episome, said episome being spontaneously lost from said cell; and

(c) a vector vehicle containing a second dominant selectable marker gene and carrying either a human GSE library or a wild-type cDNA library.

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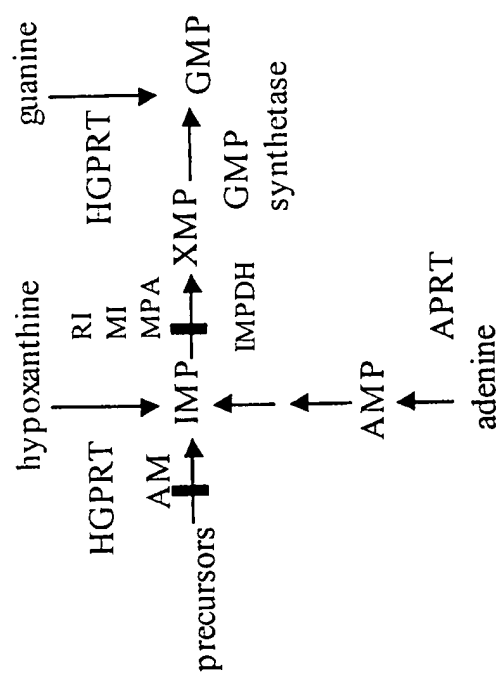


FIG. 1

FIG. 2A

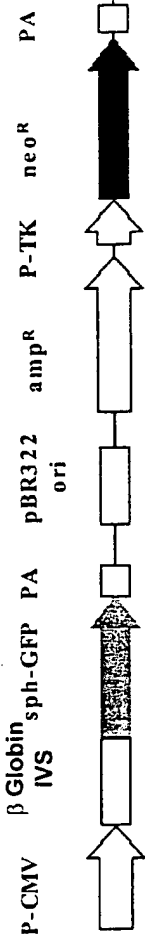
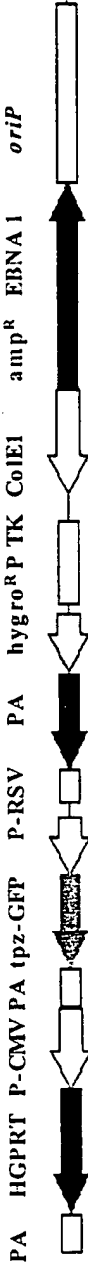


FIG. 2B



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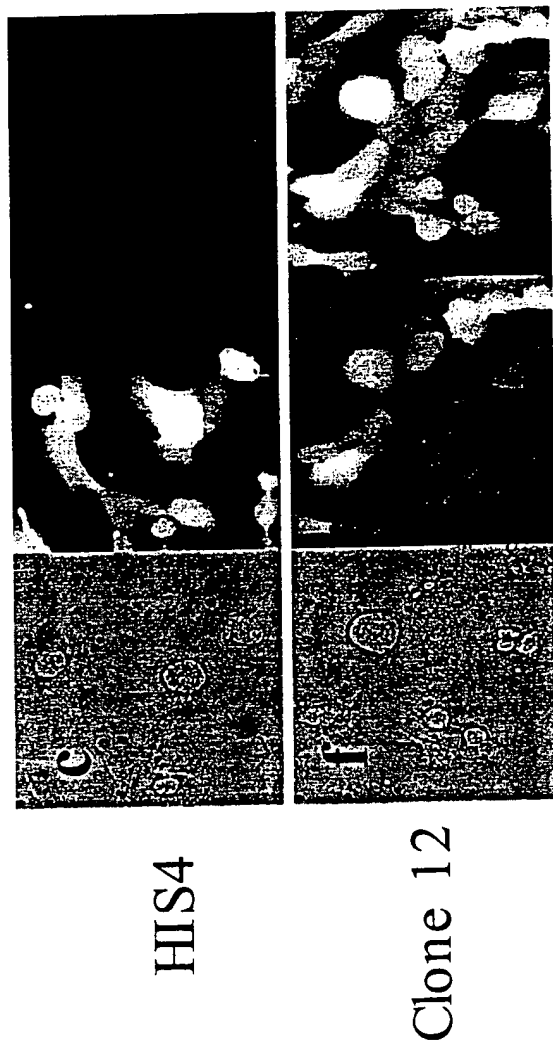


FIG. 3

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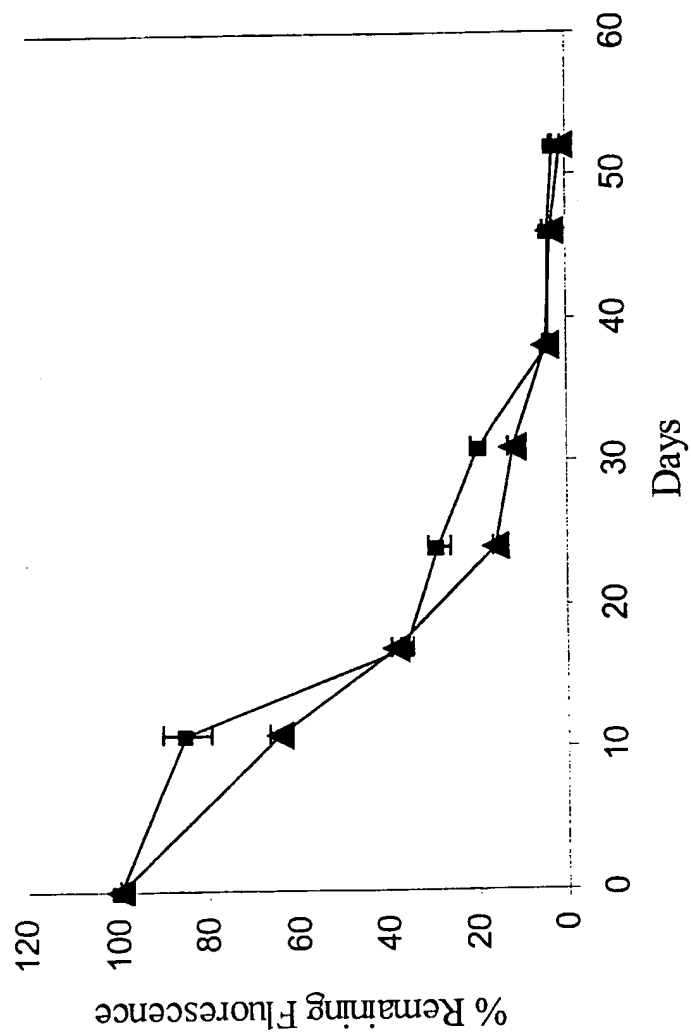


FIG. 4

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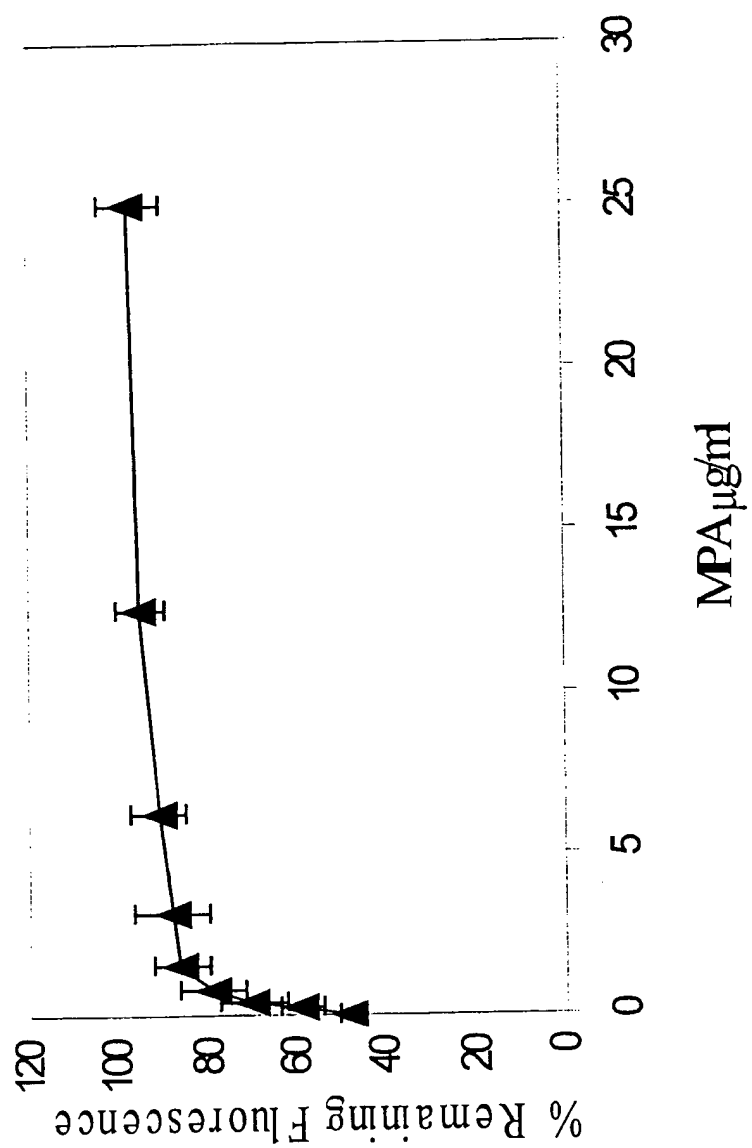


FIG. 5

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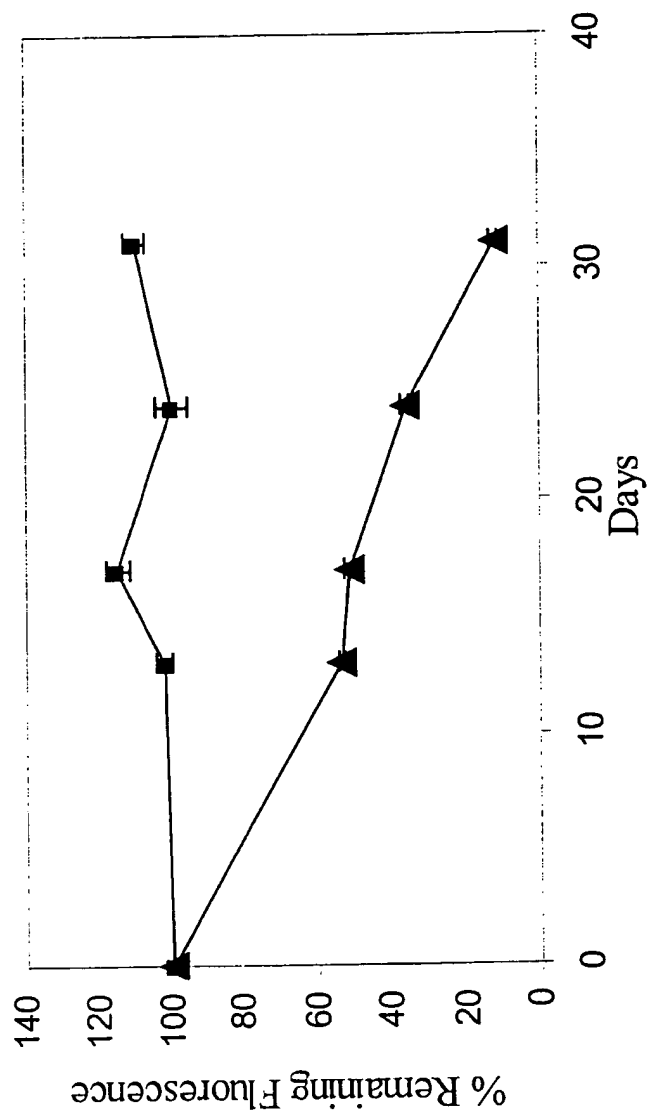


FIG. 6

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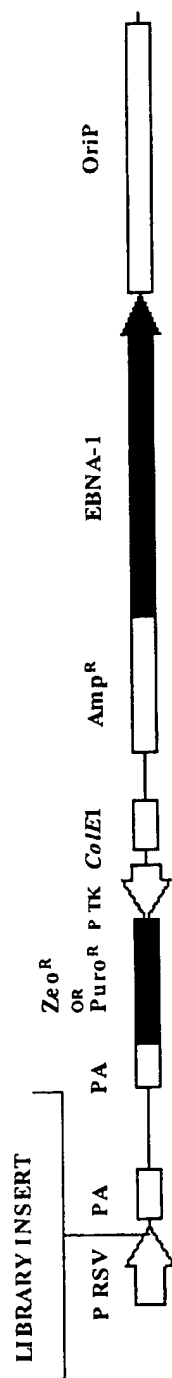


FIG. 7

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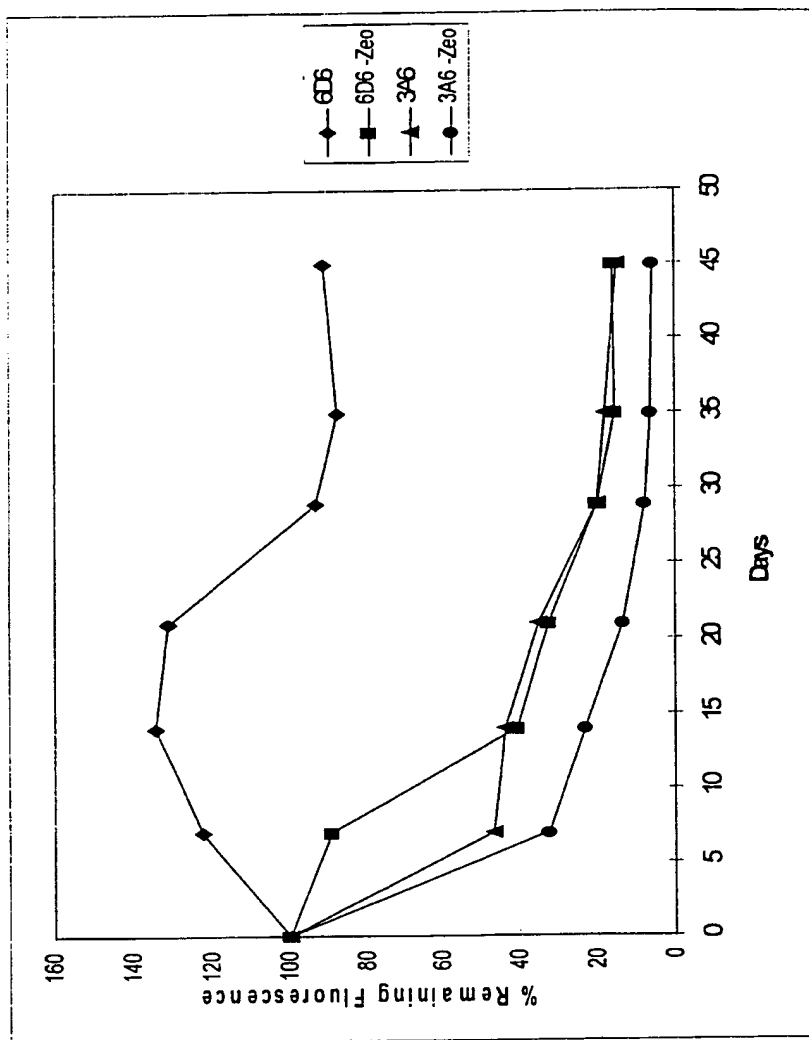


FIG. 8

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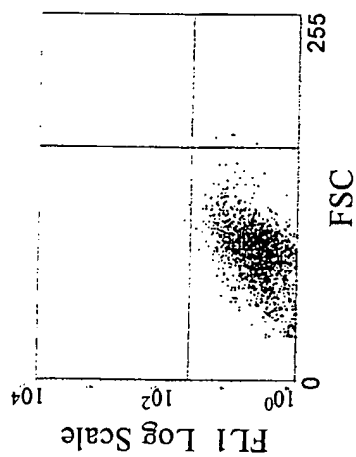


FIG. 9B

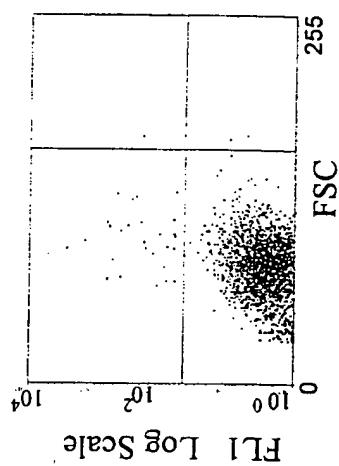


FIG. 9C

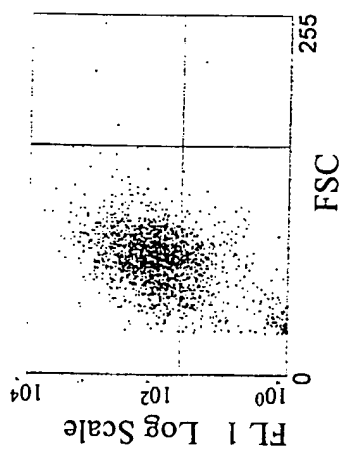


FIG. 9A

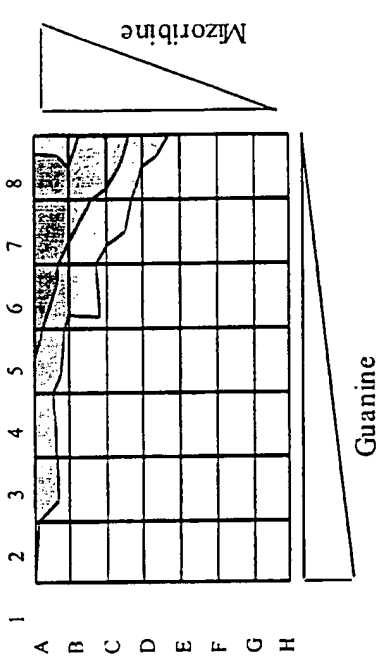


FIG. 10A

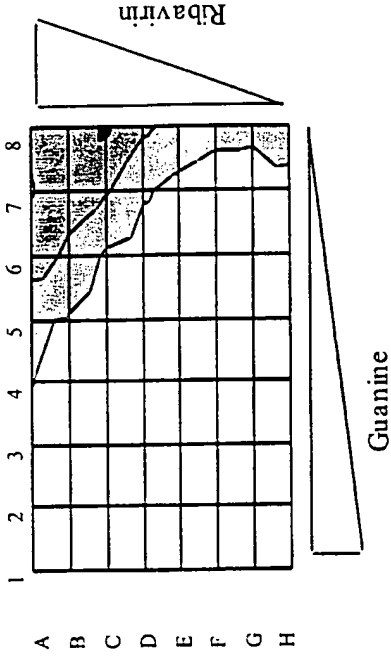


FIG. 10B

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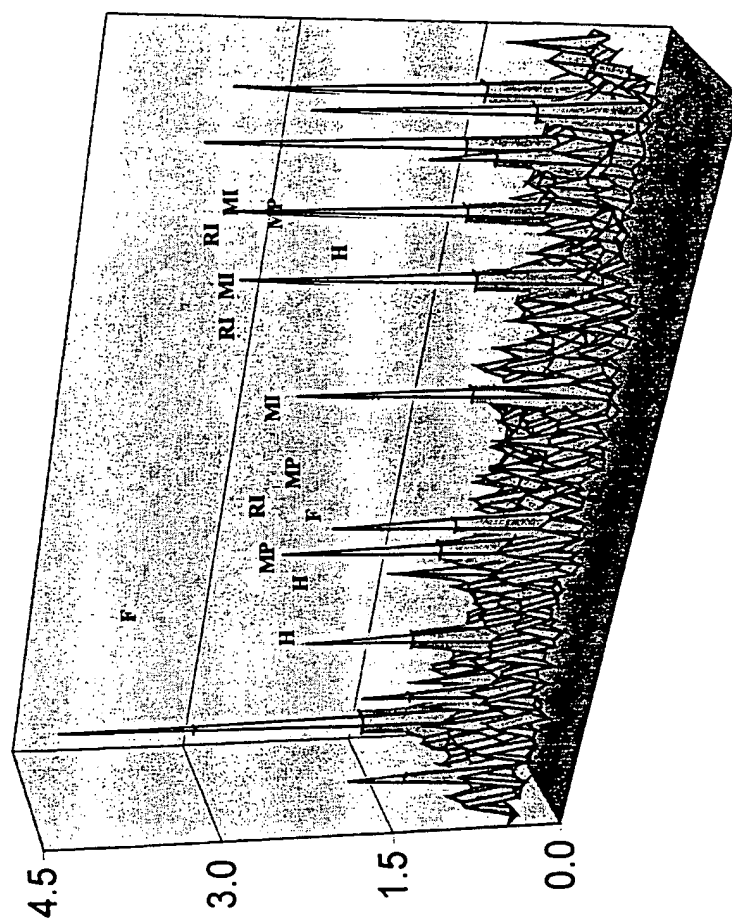


FIG. 11

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IL 00/00535

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/10 C12Q1/68 C12N15/85 //C12N15/54

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>VAN MEIR E.G. ET AL.: "Single cell monitoring of growth arrest and morphological changes induced by transfer of wild-type p53 alleles to glioblastoma cells."</p> <p>PROC. NATL. ACAD. SCI. USA, vol. 92, February 1995 (1995-02), pages 1008-1012, XP002157214</p> <p>-& Invitrogen, Vector map of pMEP4. http://www.invitrogen.com/vecgif/pmep4.gif XP002157217</p> <p style="text-align: center;">--- -/--</p>	8,9,17, 18

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

12 January 2001

Date of mailing of the international search report

29/01/2001

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Galli, I

INTERNATIONAL SEARCH REPORT

International Application No

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>CAMENISCH G.: "A polyoma-based episomal vector efficiently expresses exogenous genes in mouse embryonic stem cells." NUCL. ACIDS RES., vol. 24, no. 19, 1996, pages 3707-3713, XP002157215 cited in the application the whole document</p> <p style="text-align: center;">---</p>	8,9,17, 18
A	<p>GALLI I. ET AL.: "DNA replication and order of cell cycle events: a role for protein isoprenylation?" BIOL. CHEM., vol. 378, September 1997 (1997-09), pages 963-973, XP002157216 the whole document</p> <p style="text-align: center;">---</p>	1-43
A	<p>WO 99 24603 A (FRIEND STEPHEN ;HARTWELL LELAND (US); HUTCHINSON FRED CANCER RES ()) 20 May 1999 (1999-05-20) abstract claims 1-43</p> <p style="text-align: center;">---</p>	1-43
A	<p>CALOS M P: "The potential of extrachromosomal replicating vectors for gene therapy" TRENDS IN GENETICS,NL,ELSEVIER SCIENCE PUBLISHERS B.V. AMSTERDAM, vol. 12, no. 11, November 1996 (1996-11), pages 463-466, XP004181563 ISSN: 0168-9525 cited in the application the whole document</p> <p style="text-align: center;">-----</p>	1-43

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IL 00/00535

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9924603 A	20-05-1999	AU 1310099 A EP 1029072 A	31-05-1999 23-08-2000